



SEQUENCE LISTING

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<120> IMPROVED CONDITIONALLY REPLICATING VECTORS
FOR INHIBITING VIRAL INFECTIONS

<130> 39727-20007.00

<140> US 09/819,401
<141> 2001-03-27

<160> 18

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide encoded wild-type HIV US sequence

<400> 1
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39

<210> 2
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Vector sequence

<400> 2
gtgtgcccac ctgttgtgtg actctggcag ctagagaac

39

<210> 3
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Sequence encoded ribozyme

<400> 3
cacacaacac tcatgaggcc gaaaggccga aacgggcaca

40

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<210> 4
<211> 40
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<220>
<223> Sequence encoded ribozyme

<400> 4
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<210> 5
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<220>
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<400> 5
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<210> 6
<211> 39
<212> DNA
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<220>
<223> Vector sequence

<400> 6
gtgtccccgt ctgttgttg actctggcaa ctagagatc 39

<210> 7
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Consensus splice donor

<221> misc_feature
<222> (1)...(15)
<223> n = A,T,C or G

<400> 7
nnnnnaggtaa gtnnn 15

<210> 8
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Beta-globin splice donor

<221> misc_feature

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<222> (1)...(15)
<223> n = A,T,C or G

<400> 8
nngcaggta agtat

15

<210> 9
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV major splice donor

<221> misc_feature
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<223> n = A,T,C or G

<400> 9
nngactggtg agtan

15

<210> 10
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-1 env splice donor

<400> 10
aaagcagtaa gtagt

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<210> 11
<211> 15
<212> DNA
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<220>
<223> HIV-2 env splice donor

<400> 11
agacaagtga gtaag

15

<210> 12
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> HIV-2 major splice donor

<221> misc_feature
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<223> n = A,T,C or G

<400> 12
nngaaggtaa gtgcn

15

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<210> 13
<211> 112
<212> DNA
<213> Artificial Sequence

<220>
<223> Double-stranded oligonucleotide

<400> 13
aagcttgcct tgagtgcctca aagttagtgtg tgcccacctg ttgtgtgact ctggcagcta      60
gagatccac agaccctttt agtcagtgtg gaaaatctct agcagtggcg cc      112

<210> 14
<211> 39
<212> DNA
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<220>
<223> Oligonucleotide with mutant nucleotides

<221> misc_feature
<222> (1)...(39)
<223> n = A,T,C or G

<400> 14
gtgtgccnn ctgttgttg actctggnn ctagaganc      39

<210> 15
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<212> DNA
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<223> Mutated oligonucleotide

<400> 15
gtgtgcccat ctgttgttg actctggtaa ctagagatc      39

<210> 16
<211> 39
<212> DNA
<213> Artificial Sequence

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<223> Mutated oligonucleotide

<400> 16
gtgtgccgt ctgttgttg actctggtag ctagagatc      39

<210> 17
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<212> DNA
<213> Artificial Sequence

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<223> Analog splice donor

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<221> misc_feature
<222> (1)...(16)
<223> n = A,T,C or G

<400> 17
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<210> 18
<211> 1185
<212> PRT
<213> Artificial Sequence

<220>
<223> Amino acid sequence of a chimeric HIV CTL epitope

<400> 18
Met Lys Ile Arg Leu Arg Pro Gly Gly Asn Lys Lys Tyr Lys Leu Lys
1 5 10 15
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Gly Ser Glu Glu
20 25 30
Leu Arg Ser Leu Tyr Asn Thr Val Ala Val Leu Tyr Cys Val His Gln
35 40 45
Lys Ile Glu Val Lys Asp Thr Lys Glu Ala Leu Asp Thr Glu Asn Arg
50 55 60
Asn Gln Glu Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gly Gln Met
65 70 75 80
Val His Gln Ala Leu Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
85 90 95
Ile Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
100 105 110
Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
115 120 125
Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Ala Thr Ile Asn
130 135 140
Glu Glu Ala Ala Glu Trp Asp Arg Leu His Pro Val His Ala Gly Pro
145 150 155 160
Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Thr Ser Thr Leu Gln
165 170 175
Glu Gln Ile Ala Trp Met Thr Asn Asn Pro Pro Ile Pro Val Gly Glu
180 185 190
Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys Ile Val Arg Met
195 200 205
Tyr Ser Pro Val Ser Ile Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
210 215 220
Thr Leu Arg Ala Glu Gln Ala Thr Gln Glu Val Lys Asn Trp Met Thr
225 230 235 240
Glu Thr Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu
245 250 255
Lys Ala Leu Leu Glu Asp Met Met Thr Ala Cys Gln Gly Val Gly Gly
260 265 270
Pro Gly His Lys Ala Arg Leu Val Gln Glu Gly His Gln Met Lys Asp
275 280 285
Cys Thr Glu Arg Gln Ala Asn Phe Gly Asn Phe Pro Gln Ser Arg Leu
290 295 300
Glu Pro Thr Ala Pro Pro Glu Ile Thr Leu Trp Gln Arg Pro Leu Val
305 310 315 320

Asp Thr Val Leu Glu Asp Met Asn Leu Val Leu Val Gly Pro Thr Pro
 325 330 335
 Val Asn Ile Ser Pro Ile Glu Thr Val Pro Val Lys Leu Gly Pro Lys
 340 345 350
 Val Lys Gln Trp Pro Leu Ala Leu Val Glu Ile Cys Thr Glu Met Glu
 355 360 365
 Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Thr Val Leu Asp Val Gly
 370 375 380
 Asp Ala Tyr Phe Ser Val Pro Leu Asp Glu Asp Phe Arg Lys Tyr Thr
 385 390 395 400
 Ala Phe Thr Ile Pro Ser Ile Trp Lys Gly Ser Pro Ala Ile Phe Gln
 405 410 415
 Ser Ser Met Thr Lys Asn Pro Asp Ile Val Ile Tyr Gln Tyr Met Asp
 420 425 430
 Asp Leu Tyr Val Asp Leu Glu Glu Gly Gln His Arg Thr Lys Ile Glu
 435 440 445
 Glu Leu Arg Gln His Leu Leu Arg Trp Gly Phe Thr Thr Pro Asp Lys
 450 455 460
 Lys Pro Ile Lys Leu Pro Glu Lys Glu Ser Trp Leu Val Gly Lys Leu
 465 470 475 480
 Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys Val Lys Gln Leu Ile
 485 490 495
 Pro Ile Thr Glu Glu Ala Glu Leu Glu Ile Leu Lys Glu Pro Val His
 500 505 510
 Gly Val Tyr Gln Ile Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly
 515 520 525
 Asp Val Lys Gln Leu Thr Glu Ala Val Lys Ile Thr Thr Glu Ser Ile
 530 535 540
 Val Ile Trp Pro Ile Gln Lys Glu Thr Trp Glu Thr Trp Trp Thr Glu
 545 550 555 560
 Tyr Trp Pro Leu Val Lys Leu Trp Tyr Gln Leu Glu Pro Ile Val Gly
 565 570 575
 Ala Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Lys Ala Leu Gln Asp
 580 585 590
 Ser Gly Leu Glu Val Asn Ile Val Thr Asp Ser Gln Tyr Ala Leu Gly
 595 600 605
 Ile Glu Ser Glu Leu Val Ser Gln Ile Ile Glu Gln Leu Leu Ala Trp
 610 615 620
 Val Pro Ala His Lys Gly Tyr Glu Glu Ala Glu Val Ile Glu Thr Ala
 625 630 635 640
 Tyr Phe Ile Leu Lys Leu Leu Trp Lys Gly Glu Gly Ala Val Ile
 645 650 655
 Ser Gly Trp Ile Leu Asn Thr Tyr Arg Val Lys Gly Ile Arg Lys Asn
 660 665 670
 Tyr Ala Glu Asn Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp
 675 680 685
 Lys Glu Ala Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr
 690 695 700
 Asp Pro Asn Pro Gln Glu Val Val Leu His Glu Asp Ile Ile Ser Leu
 705 710 715 720
 Trp Asp Gln Ser Leu Lys Lys Leu Thr Pro Leu Cys Val Thr Leu Asn
 725 730 735
 Cys Ser Phe Asn Val Thr Thr Leu Ile Asn Thr Ser Tyr Thr Leu Ile
 740 745 750
 Asn Cys Lys Ser Ser Thr Ile Thr Gln Ala Cys Pro Lys Cys Lys Asn
 755 760 765
 Val Ser Thr Val Gln Cys Arg Pro Val Val Ser Thr Gln Leu Leu Leu

770	775	780
Asn	Gly	Ser
Leu	Ala	Glu
Glu	Asp	Ile
Val	Ser	Ile
Ile	Glu	Ile
Asn	Cys	
785	790	795
Thr	Arg	Pro
Asn	Asn	Asn
Asn	Thr	Arg
Lys	Lys	Ile
Thr	Leu	Gly
Pro	Gly	
805	810	815
Arg	Val	Leu
Tyr	Thr	Thr
Gly	Glu	Asn
Asn	Asn	Thr
Thr	Leu	Lys
Leu	Gln	Ile
Gln	Ile	Val
Phe	Lys	Met
Lys	Arg	His
Glu	Ile	
835	840	845
Ser	Phe	Asn
Cys	Gly	Gly
Gly	Glu	Phe
Phe	Tyr	Cys
Asn	Ser	Thr
Thr	Gln	Leu
850	855	860
Phe	Leu	Pro
Cys	Arg	Ile
Lys	Gln	Ile
Ile	Asn	Arg
Arg	Trp	Gln
Glu	VaL	
865	870	875
Gly	Lys	Ala
Ala	Met	Tyr
Met	Ala	Pro
Pro	Ile	Glu
Gly	Gly	Gln
Gln	Ile	Arg
Ile	Arg	Cys
Leu		Leu
885	890	895
Ser	Asn	Ile
Thr	Gly	Val
Val	Lys	Ile
Glu	Pro	Leu
Leu	Gly	Val
Ala	Pro	Thr
900	905	910
Lys	Ala	Lys
Arg	Arg	Val
Arg	Val	Val
Gln	Arg	Arg
Ala	Ile	Glu
Ile	Glu	Ala
Gln	Gln	Gln
915	920	925
His	Leu	Gly
Ile	Lys	Gln
Leu	Gln	Ala
Ala	Arg	Val
Arg	Val	Ala
Glu	Arg	
930	935	940
Tyr	Leu	Lys
Asp	Gln	Gln
Gln	Leu	Leu
Leu	Gly	Ile
Gly	Ile	Thr
Thr	Val	Pro
Pro	Trp	Asn
945	950	955
960		
Ala	Ser	Trp
Trp	Tyr	Ile
Tyr	Ile	Lys
Ile	Phe	Ile
Met	Ile	Val
Ile	Gly	Val
Leu		
965	970	975
Ser	Ile	Val
Asn	Arg	Val
Arg	Val	Gln
Gly	Tyr	Ser
Tyr	Ser	Pro
Pro	Leu	Phe
Phe	Gln	
980	985	990
Thr	His	Arg
Leu	Val	Asp
Asp	Gly	Phe
Gly	Leu	Thr
Leu	Leu	Leu
Ala	Ile	Arg
Ile	Gly	Arg
Gly	Arg	Gly
Arg	Gly	Trp
Trp	Ala	Ala
Ala	1010	1015
1020		
Leu	Lys	Tyr
Ser	Leu	Leu
Asn	Ala	Thr
Ala	Ile	Ala
Ala	Val	Asp
Asp	Arg	Val
1025	1030	1035
1040		
Ile	Glu	Ile
Ile	Val	Gln
Gln	Arg	Thr
Arg	Cys	Arg
Ala	Ile	Leu
Leu	His	Ile
His	Pro	Arg
1045	1050	1055
Arg	Ile	Arg
Gln	Gly	Leu
Leu	Glu	Arg
Arg	Ala	Leu
Ala	Leu	Trp
Leu	Trp	Pro
Pro	Ala	Ile
1060	1065	1070
Glu	Arg	Met
Arg	Val	Gly
Gly	Phe	Pro
Pro	Val	Arg
Val	Arg	Pro
Arg	Pro	Gln
Gly	Gly	Val
1075	1080	1085
Met	Thr	Tyr
Tyr	Lys	Ala
Ala	Ala	His
His	Asp	Leu
Asp	Leu	Ser
Ser	His	Phe
Phe	Leu	Lys
Lys	Glu	
1090	1095	1100
Gly	Gly	Leu
Leu	Glu	Gly
Gly	Leu	Ile
Ile	Tyr	Ser
Ser	Gln	Lys
Gln	Lys	Arg
Arg	Gly	Gln
Gly	Gln	Asp
Asp	Ile	Leu
1105	1110	1115
1120		
Asp	Leu	Trp
Trp	Val	Tyr
Tyr	His	Thr
His	Gln	Gly
Gly	Phe	Phe
Phe	Phe	Pro
Pro	Asp	Trp
Asp	Trp	Gln
1125	1130	1135
Tyr	Thr	Pro
Pro	Gly	Gly
Gly	Thr	Arg
Arg	Tyr	Pro
Tyr	Pro	Leu
Leu	Cys	Phe
Cys	Phe	Trp
Trp	Cys	
1140	1145	1150
Phe	Lys	Leu
Leu	Val	Pro
Pro	Val	Val
Val	Leu	Met
Met	Trp	Lys
Lys	Phe	Asp
Asp	Ser	Lys
Lys	Leu	
1155	1160	1165
Ala	Phe	His
His	His	Val
His	Val	Ala
Ala	Arg	Glu
Glu	Leu	His
His	Pro	Glu
Glu	Tyr	Phe
Phe	Lys	Asp
Asp	1170	1175
1180		
Cys		
1185		